10/056,483 (Zwital)

	Type	Hits	Search Text	DBs	Time Stamp	Comments	Error Definition	Errors	Ref #
1	BRS	1	image same (differential adj1 (gene protein) adj1 expression) same ((match$3 associat$3) with (linear adj1 (regression fit$4)))	US-PGPUB; USPAT; EPO; JPO; DERWENT; IBM_TDB	2005/03/11 14:33				S1
2	BRS	1	image same (gene protein DNA) same ((match$3 associat$3) with (linear adj1 (regression fit$4)))	US-PGPUB; USPAT; EPO; JPO; DERWENT; IBM_TDB	2005/03/11 14:36				S2
3	BRS	6	((pattern template) with (match$3 associat$3) with (linear adj1 (regression fit$4)))	US-PGPUB; USPAT; EPO; JPO; DERWENT; IBM_TDB	2005/03/14 16:01				S3
4	BRS	3184	382/129,130,151,152,181,209.ccls.	US-PGPUB; USPAT; EPO; JPO; DERWENT; IBM_TDB	2005/03/15 12:01				S4
5	BRS	2525	S4 and @ad<"20010129"	US-PGPUB; USPAT; EPO; JPO; DERWENT; IBM_TDB	2005/03/11 15:59				S5
6	BRS	38	S5 and ((gene protein DNA RNA) with (match$3 associat$3 register$3))	US-PGPUB; USPAT; EPO; JPO; DERWENT; IBM_TDB	2005/03/11 14:44				S6
7	BRS	6	S5 and ((gene protein DNA RNA) and (linear adj1 (regression fit$4)))	US-PGPUB; USPAT; EPO; JPO; DERWENT; IBM_TDB	2005/03/11 14:45				S7
8	BRS	10	("20020028021" | "20030068082" | "5208870" | "6245517" | "6251601" | "6285449" | "6319682" | "6404925" | "6411741" | "6564082").PN.	US-PGPUB; USPAT; USOCR	2005/03/11 15:37				S8
9	BRS	9	("5001766" | "5487115" | "5627912" | "5837475" | "5916747" | "6349144" | "6362832" | "6498863" | "6571005").PN.	US-PGPUB; USPAT; USOCR	2005/03/11 15:41				S9
10	BRS	77	((pattern template object character) with (match$3 recognition) with (linear$2 near3 (regress$3 fit$4)))	US-PGPUB; USPAT; EPO; JPO; DERWENT; IBM_TDB	2005/03/11 16:10				S10
11	BRS	29	S10 and @ad<"20010129"	US-PGPUB; USPAT; EPO; JPO; DERWENT; IBM_TDB	2005/03/11 16:11				S11

3/15/05, EAST Version: 2.0.1.4

|	Type	Hits	Search Text	DBs	Time Stamp	Comments	Error Definition	Errors	Ref #
12	BRS	30	((signal) with (match$3 recognition register$3correlat$3) with (linear$2 near3 (regress$3 fit$4)))	US-PGPUB; USPAT; EPO; JPO; DERWENT; IBM_TDB	2005/03/11 16:11				S12
13	BRS	11	S12 and @ad<"20010129"	US-PGPUB; USPAT; EPO; JPO; DERWENT; IBM_TDB	2005/03/11 16:11				S13
14	BRS	1883	(correlat$3 with (LMS (least$1square$1) (linear adj1 (regression fit$4))))	US-PGPUB; USPAT; EPO; JPO; DERWENT; IBM_TDB	2005/03/14 10:49				S14
15	BRS	1328	(correlat$3 with (linear adj1 (regression fit$4)))	US-PGPUB; USPAT; EPO; JPO; DERWENT; IBM_TDB	2005/03/14 10:50				S15
16	BRS	51	(pattern same (correlat$3 with (linear adj1 (regression fit$4))))	US-PGPUB; USPAT; EPO; JPO; DERWENT; IBM_TDB	2005/03/14 10:50				S16
17	BRS	15	S16 and @ad<"20010129"	US-PGPUB; USPAT; EPO; JPO; DERWENT; IBM_TDB	2005/03/14 11:21				S17
18	BRS	2	EP-848067-$.did.	US-PGPUB; USPAT; EPO; JPO; DERWENT; IBM_TDB	2005/03/14 11:23				S18
19	IS&R	5	("6600996").PN.	US-PGPUB; USPAT; EPO; JPO; DERWENT; IBM_TDB	2005/03/14 11:53				S19
20	BRS	1887	(differential adj1 (gene protein) adj1 expression)	US-PGPUB; USPAT; EPO; JPO; DERWENT; IBM_TDB	2005/03/14 16:05				S20
21	BRS	184	micro$1array same (differential adj1 (gene protein) adj1 expression)	US-PGPUB; USPAT; EPO; JPO; DERWENT; IBM_TDB	2005/03/14 16:05				S21

	Type	Hits	Search Text	DBs	Time Stamp	Comments	Error Definition	Errors	Ref #
22	BRS	6	micro$1array same match$3 same (differential adj1 (gene protein) adj1 expression)	US-PGPUB; USPAT; EPO; JPO; DERWENT; IBM_TDB	2005/03/14 16:06				S22
23	BRS	31078	435/6,91.1,287.1.ccls.	US-PGPUB; USPAT; EPO; JPO; DERWENT; IBM_TDB	2005/03/15 11:48				S23
24	BRS	16772	S23 and @ad<"20010129"	US-PGPUB; USPAT; EPO; JPO; DERWENT; IBM_TDB	2005/03/15 11:49				S24
25	BRS	286	S24 and (linear adj1 (regress$3 fit$4))	US-PGPUB; USPAT; EPO; JPO; DERWENT; IBM_TDB	2005/03/15 11:50				S25
26	BRS	16	S24 and (expression same (linear adj1 (regress$3 fit$4)))	US-PGPUB; USPAT; EPO; JPO; DERWENT; IBM_TDB	2005/03/15 11:50				S26
27	BRS	700	382/128.ccls. and @ad<"20010129"	US-PGPUB; USPAT; EPO; JPO; DERWENT; IBM_TDB	2005/03/15 12:02				S27
28	BRS	3	S27 and (expression same (linear adj1 (regress$3 fit$4)))	US-PGPUB; USPAT; EPO; JPO; DERWENT; IBM_TDB	2005/03/15 12:06				S28

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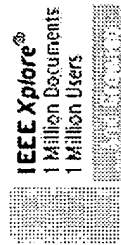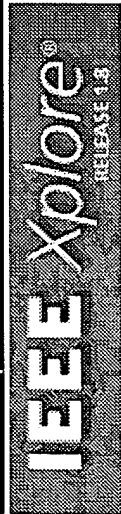
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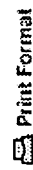
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1 **Linear least squares compartmental-model-independent parameter identification in PET**
Thie, J.A.; Smith, G.T.; Hubner, K.F.;
Medical Imaging, IEEE Transactions on , Volume: 16 , Issue: 1 , Feb. 1997
Pages:11 - 16

[Abstract]   [PDF Full-Text (128 KB)]   **IEEE JNL**

2 **The fuzzy regression approach to peak load estimation in power distribution systems**
Nazarko, J.; Zalewski, W.;
Power Systems, IEEE Transactions on , Volume: 14 , Issue: 3 , Aug. 1999
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[Abstract]   [PDF Full-Text (488 KB)]   **IEEE JNL**

3 **Identification of probabilistic system uncertainty regions by explicit evaluation of bias and variance errors**

Hakvoort, R.G.; Van den Hof, M.J.;
Automatic Control, IEEE Transactions on , Volume: 42 , Issue: 11 , Nov. 1997
Pages:1516 - 1528

[Abstract]   [PDF Full-Text (580 KB)]   **IEEE JNL**

4 **Maximum likelihood parameter and rank estimation in reduced-rank multivariate linear regressions**
Stoica, P.; Viberg, M.;
Signal Processing, IEEE Transactions on [see also Acoustics, Speech, and Signal Processing, IEEE Transactions on] , Volume: 44 , Issue: 12 , Dec. 1996
Pages:3069 - 3078

[Abstract]   [PDF Full-Text (904 KB)]   **IEEE JNL**

5 **An efficient method for determining threshold voltage, series resistance and effective geometry of MOS transistors**
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Semiconductor Manufacturing, IEEE Transactions on , Volume: 9 , Issue: 2 , May 1996
Pages:215 - 222

[Abstract]   [PDF Full-Text (784 KB)]   **IEEE JNL**

6 **Performance analysis of general tracking algorithms**
Lei Guo; Lennart Ljung;
Automatic Control, IEEE Transactions on , Volume: 40 , Issue: 8 , Aug. 1995
Pages:1388 - 1402

[Abstract]   [PDF Full-Text (940 KB)]   **IEEE JNL**

7 **Correlating radar backscatter with components of biomass in loblolly pine forests**
Kasischke, E.S.; Christensen, N.L., Jr.; Bourgeau-Chavez, L.L.;
Geoscience and Remote Sensing, IEEE Transactions on , Volume: 33 , Issue: 3 , May 1995
Pages:643 - 659

[Abstract]   [PDF Full-Text (1344 KB)]   **IEEE JNL**

8 **System identification using Kautz models**
Wahlberg, B.;

Automatic Control, IEEE Transactions on , Volume: 39 , Issue: 6 , June 1994
Pages:1276 - 1282

[Abstract]   [PDF Full-Text (524 KB)]   **IEEE JNL**

9 **Wheelchair impact response to ISO test pendulum and ISO standard curb**
Cooper, R.A.; Robertson, R.N.; VanSickle, D.P.; Stewart, K.J.; Albright, S.J.;
Rehabilitation Engineering, IEEE Transactions on [see also IEEE Trans. on Neural
Systems and Rehabilitation] , Volume: 2 , Issue: 4 , Dec. 1994
Pages:240 - 246

[Abstract]   [PDF Full-Text (652 KB)]   **IEEE JNL**

10 **Kinematic model relating complex 2D smooth pursuit eye movements and Purkinje cell firing rate in cerebellar flocculus and paraflocculus of the rhesus monkey**
Minah Suh; Hoi-Chung Leung; Kettner, R.E.;
Engineering in Medicine and Biology society, 1997. Proceedings of the 19th Annual
International Conference of the IEEE , Volume: 4 , 30 Oct.-2 Nov. 1997
Pages:1488 - 1491 vol.4

[Abstract]   [PDF Full-Text (332 KB)]   **IEEE CNF**

11 **Ultrasonic spectrum analysis for assays of different scatterer morphologies: theory and very-high frequency clinical results**
Lizzi, F.L.; Astor, M.; Kalisz, A.; Liu, T.; Coleman, D.J.; Silverman, R.; Ursea, R.; Rondeau, M.;
Ultrasonics Symposium, 1996. Proceedings., 1996 IEEE , Volume: 2 , 3-6 Nov.
1996
Pages:1155 - 1159 vol.2

[Abstract]   [PDF Full-Text (372 KB)]   **IEEE CNF**

12 **Application of least absolute value parameter estimation technique based on linear programming to short-term load forecasting**
Soliman, S.A.; Persaud, S.; El-Nagar, K.; El-Hawary, M.E.;
Electrical and Computer Engineering, 1996. Canadian Conference on , Volume:
2 , 26-29 May 1996
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[Abstract]   [PDF Full-Text (496 KB)]   **IEEE CNF**

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13 **Asymptotic probability density of the generalization error**

Poncet, A.;
Neural Networks for Identification, Control, Robotics, and Signal/Image Processing, 1996. Proceedings., International Workshop on , 21-23 Aug. 1996
Pages:66 - 74

[Abstract]   [PDF Full-Text (396 KB)]   **IEEE CNF**

14 **Reduced-rank linear regression**

Stoica, P.; Viberg, M.;
Statistical Signal and Array Processing, 1996. Proceedings., 8th IEEE Signal Processing Workshop on (Cat. No.96TB10004 , 24-26 June 1996
Pages:542 - 545

[Abstract]   [PDF Full-Text (264 KB)]   **IEEE CNF**

15 **Optical remote sounding of aerosol formations on the base of numerical simulation of the scattering radiation**

Belyaev, B.I.; Katkovsky, L.V.; Kabashnikov, V.P.; Nekrasov, V.P.;
Geoscience and Remote Sensing Symposium, 1996. IGARSS '96. 'Remote Sensing for a Sustainable Future.', International , Volume: 1 , 27-31 May 1996
Pages:19 - 21 vol.1

[Abstract]   [PDF Full-Text (280 KB)]   **IEEE CNF**

Results (page 1): microarray expression linear regression

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1 <u>Articles on microarray data mining: Statistical methods for joint data mining of gene expression and</u>
<u>DNA sequence database</u>
Marla D. Curran, Hong Liu, Fan Long, Nanxiang Ge
December 2003 **ACM SIGKDD Explorations Newsletter,** Volume 5 Issue 2

Full text available: [📄 pdf(869.45 KB)]   Additional Information: <u>full citation, abstract, references</u>

One of the purposes of microarray gene expression experiments is to identify genes regulated under specific
cellular conditions. With the availability of putative transcription factor binding motifs, it is now possible to
relate gene expression pattern to the pattern of transcription factor binding sites (TFBS), as well as study
how TFBS interact with each other to control gene expression. The objectives of this study are to develop a
systematic approach for combining data from microarray gene e ...

Keywords: T-helper cells, cluster analysis, logistic regression, microarray, modeling, regulatory motifs,
transcription factor binding site (TFBS)

2 <u>Gene selection criterion for discriminant microarray data analysis based on extreme value distributions</u>   ▨
Wentian Li, Ivo Grosse
April 2003 **Proceedings of the seventh annual international conference on Computational molecular**
biology

Full text available: [📄 pdf(158.65 KB)]   Additional Information: <u>full citation, abstract, references, index terms</u>

An important issue commonly encountered in the analysis of microarray data is to decide which and how
many genes should be selected for further studies. For discriminant microarray data analyses based on
statistical models, such as the logistic regression model, this gene selection can be accomplished by a
comparison of the maximum likelihood of the model given the real data, $L(D|M)$, and the expected
maximum likelihood of the model given an ensemble of surrogate data, $L(D0|M)$. Typical ...

Results (page 1): microarray expression linear regression

Keywords: classification, extreme values, logistic regression, microarray

3 Articles on microarray data mining: Microarray data mining: facing the challenges
Gregory Piatetsky-Shapiro, Pablo Tamayo
December 2003 **ACM SIGKDD Explorations Newsletter,** Volume 5 Issue 2

Full text available: 🗎 pdf(224.37 KB)   Additional Information: full citation, references

4 Articles on microarray data mining: Supervised analysis when the number of candidate features (p)
greatly exceeds the number of cases (n)
Richard Simon
December 2003 **ACM SIGKDD Explorations Newsletter,** Volume 5 Issue 2

Full text available: 🗎 pdf(183.08 KB)   Additional Information: full citation, abstract, references

New genomic and proteomic technologies provide measurements of thousands of features for each case.
This provides a context for enhanced discovery and false discovery. Most statistical and machine learning
procedures were not developed for the p>>n setting and the literature of DNA microarray studies contains
many examples of mis-use of analytic and computatinal methods such a cross-validation. This paper
highlights some of key aspects of p>>n problems for identifying informative fea ...

Keywords: classification, cross-validation, prediction

5 Joint classifier and feature optimization for cancer diagnosis using gene expression data
Balaji Krishnapuram, Lawrence Carin, Alexander J. Hartemink
April 2003   **Proceedings of the seventh annual international conference on Computational molecular
biology**

Full text available: 🗎 pdf(392.37 KB)   Additional Information: full citation, abstract, references, index terms

Recent research has demonstrated quite convincingly that accurate cancer diagnosis can be achieved by
constructing classifiers that are designed to compare the gene expression profile of a tissue of unknown
cancer status to a database of stored expression profiles from tissues of known cancer status. This paper
introduces the JCFO, a novel algorithm that uses a sparse Bayesian approach to jointly identify both the
optimal nonlinear classifier for diagnosis and the optimal set of genes on which t ...

Keywords: JCFO, RVM, SVM, classication, disease diagnosis, feature selection, joint optimization, sparse
bayesian methods

6 Articles on microarray data mining: A novel approach to determine normal variation in gene
expression data
Vinay Nadimpally, Mohammed J. Zaki

Results (page 1): microarray expression linear regression

December 2003 **ACM SIGKDD Explorations Newsletter**, Volume 5 Issue 2

Full text available: 📄 pdf(186.46 KB)   Additional Information: full citation, abstract, references

Animal models for human diseases are of crucial importance for studying gene expression and regulation. In the last decade the development of mouse models for cancer, diabetes, neuro-degenerative and many other diseases has been on steady rise. Microarray analysis of patterns of gene expression in mouse models of various pathological types and the study of molecular level changes as a result of interventions, holds lot of promise to the understanding of biological processes involved. The genes w ...

Keywords: gene expression, hypertension, immune response, mouse models, normal variance, principal component analysis, replicates

7   Machine learning in DNA microarray analysis for cancer classification
Sung-Bae Cho, Hong-Hee Won
January 2003 **Proceedings of the First Asia-Pacific bioinformatics conference on Bioinformatics 2003 - Volume 19**

Full text available: 📄 pdf(405.54 KB)   Additional Information: full citation, abstract, references, citings, index terms

The development of microarray technology has supplied a large volume of data to many fields. In particular, it has been applied to prediction and diagnosis of cancer, so that it expectedly helps us to exactly predict and diagnose cancer. To precisely classify cancer we have to select genes related to cancer because extracted genes from microarray have many noises. In this paper, we attempt to explore many features and classifiers using three benchmark datasets to systematically evaluate the perf ...

Keywords: KNN, MLP, SASOM, SVM, biological data mining, classification, ensemble classifier, feature selection, gene expression profile

8   Articles on microarray data mining: Loss-based estimation with cross-validation: applications to microarray data analysis
Sandrine Dudoit, Mark J. van der Laan, Sündüz Keleş, Annette M. Molinaro, Sandra E. Sinisi, Siew Leng Teng
December 2003 **ACM SIGKDD Explorations Newsletter**, Volume 5 Issue 2

Full text available: 📄 pdf(325.39 KB)   Additional Information: full citation, abstract, references

Current statistical inference problems in genomic data analysis involve parameter estimation for high-dimensional multivariate distributions, with typically unknown and intricate correlation patterns among variables. Addressing these inference questions satisfactorily requires: (i) an intensive and thorough search of the parameter space to generate good candidate estimators; (ii) an approach for selecting an optimal estimator among these candidates; and (iii) a method for reliably assessing the ...

Keywords: censored data, classification, comparative genomic hybridization, cross-validation, density estimation, estimation, loss function, microarray, model selection, multivariate outcome, prediction, regression trees, risk, survival analysis, variable selection